

*Shukla, Ram*

# ENTERED



1600

## RAW SEQUENCE LISTING

DATE: 03/10/2003

PATENT APPLICATION: US/08/984,178

TIME: 15:40:04

Input Set : N:\Crf3\RULE60\08984178.RAW.txt

Output Set: N:\CRF4\03102003\H984178.raw

## SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Horvitz, H. Robert

6 Yuan, Junying

7 Shaham, Shai

9 (ii) TITLE OF INVENTION: CLONING, SEQUENCING AND CHARACTERIZATION

10 OF TWO CELL DEATH GENES AND USES THEREFOR

12 (iii) NUMBER OF SEQUENCES: 28

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Fish & Richardson P.C.

16 (B) STREET: 225 Franklin Street

17 (C) CITY: Boston

18 (D) STATE: MA

19 (E) COUNTRY: USA

20 (F) ZIP: 02110-2804

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk

24 (B) COMPUTER: IBM PC compatible

25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

28 (vi) CURRENT APPLICATION DATA:

C--> 29 (A) APPLICATION NUMBER: US/08/984,178

C--> 30 (B) FILING DATE: 03-Dec-1997

W--> 35 (C) CLASSIFICATION: 424

40 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: US/08/287,669

34 (B) FILING DATE: 09-AUG-1994

37 (A) APPLICATION NUMBER: US 07/979,638

38 (B) FILING DATE: 20-NOV-1992

41 (A) APPLICATION NUMBER: US 07/897,788

42 (B) FILING DATE: 12-JUN-1992

44 (viii) ATTORNEY/AGENT INFORMATION:

45 (A) NAME: Clark, Paul T.

46 (B) REGISTRATION NUMBER: 30,162

47 (C) REFERENCE/DOCKET NUMBER: 01977/198005

49 (ix) TELECOMMUNICATION INFORMATION:

50 (A) TELEPHONE: 617/542-5070

51 (B) TELEFAX: 617/542-8906

52 (C) TELEX: 200154

54 (2) INFORMATION FOR SEQ ID NO: 1:

56 (i) SEQUENCE CHARACTERISTICS:

57 (A) LENGTH: 4407 base pairs

58 (B) TYPE: nucleic acid

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```

59          (C) STRANDEDNESS: single
60          (D) TOPOLOGY: linear
W--> 62      (ii) MOLECULE TYPE: DNA
64          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
66 GAATTCGCGT CGAATCATTG TCTGTTCCGGT ATCGATTTCAG AAACCGAAAC TTGTGATCGA      60
68 TAACAAGTCA TTCAAACACG GCGAAGATGT CTATGCGTAT AACAGAATAT TTGGAGAAAT      120
70 GCTCGCAAAA CTCGAAATTG TCACCGATAA AATGATTAAC TTGAAGGGGC TAATGTAAGT      180
72 TATCTGATGT TTCTACAATT AAAAAAATTG TTTTTTTTTT CAAATTAATT TTCGAAGATT      240
74 AACGAAAAAC GATTAAAAAT CAATAAAACG CAATAAAGAG GGCTTGGCTT TCTTTTAAAT      300
76 TTAAATTATA ATTTTCTGTA TTGTTGTATG AAGCTACAAA ATGTACTGTT TTTGTATTTG      360
78 AATATTGTAT TACAGGGTTG GGATTCTCGG CAAATATCAG CGACAGTGGG AGATTTAGAA      420
80 GAAGGACGTG TGACAATCAC TAAGTCAAAG AGGGAAGGGA TAAAGGATTG TGATATTTCA      480
82 CTGTTTACTT CATTGCTTTT TTAAATAAGA ACTATATGCC GATTTGCCGA TATATTTTGT      540
84 TTTATTAGGC CTCTCACATT CCTGTACAAT GTTTCTACCA AATAAACTGC ATTTTATCTT      600
86 GAAAAATCGA ATTTATTTTT GTCTACTTTT TACTCGTTGC ATTCGAGATC AGCATATCTT      660
88 CCGGTCTATT TATATTCAAC GATTTTATAA AATTAGTACT CCTTCATGTT TAATTTCAAT      720
90 TTATCTGTAA GCTTACTGTG ATTTTTTTAA AATCTTCTT GCTTCTATCT GATTATACAA      780
92 TGTCTTTTAC TCATTTTCAA GGTATTTTAA TGCCTCACAA TTTATGCACA TTTCGGGCTT      840
94 GGAGATTATC CCTCTATATT ACATGCCTGT TTTTTTAAAG GATATAATGT TTAACAAATA      900
96 ATTTTTTATC AATGCTATTG TATATTCTCC AGCTAACCGT TGTTTCGAAA ACATCACCTA      960
98 GCATTTTAAA ATTCACAAAA TCTTGCTTCC TTATAATCAA GAAGATTTTT CAGATGCTCT      1020
100 GCGAAATCGA ATGCCGCGCT TTGAGCACGG CACACACGAG GCTCATCCAC GACTTTGAAC      1080
102 CACGTGACGC ATTGACTTAT TTAGAAGGCA AAAACATTTT CACAGAAGAT CATTCTGAAC      1140
104 TTATCAGTAA AATGTCAACT CGCCTCGAGA GGATCGCCAA TTTTCTTCGA ATCTATCGAC      1200
106 GTCAAGCTTC TGAACCTGGA CCACTCATCG ACTTTTTCAA CTACAACAAT CAAAGTCACC      1260
108 TTGCTGATTT CCTCGAAGAC TACATCGATT TTGCGATAAA TGAGCCAGAT CTACTTCGTC      1320
110 CAGTAGTGAT TGCTCCACAA TTTTCCCGAC AAATGCTCGA TAGGAACTA TTGCTTGGGA      1380
112 ATGTTCCAAA ACAAATGACA TGCTATATTC GAGAGTATCA CGTGGATCGA GTGATCAAAA      1440
114 AGCTCGACGA GATGTGTGAT TTAGGTGAGA AAACGTGAAG CTCTCGTGTT TATTATAATC      1500
116 TTGCTTAAAC TTGACGACTC TTTTCTGTGT TTCTACACGG CCGAGCTGGA TCCGGAATAA      1560
118 CAGTAATTGC ATCACAAGCT CTTTCGAAAT CTGACCAACT TATTGGAATG TGAGTGGTAT      1620
120 TATCTGAATC TACGGATCTT CATTCTATTA CAGAAATTAT GATTCAATCG TTTGGCTCAA      1680
122 AGATAGTGGA ACAGCTCCAA AATCTACATT CGATTTATTT ACGGATATTT TGCTGATGCT      1740
124 AAAGTGAGTG AATAGAGTGC ATGTAACATT CAGCATGATT TTGAAATTAT GAAAATTTGA      1800
126 CCTGGTTAGC TTTTAATTTG ATATTTCGTG ACGCTTGCAT GTTTTGTGTG TTTGAAGACG      1860
128 AGCCCGTGTT GTGAGCGACA CGGATGACTC GCATTCGATC ACCGACTTCA TTAACCGTGT      1920
130 TCTTTCAAGA AGCGAAGACG ATCTTCTCAA TTTCCCATCG GTGGAGCATG TCACGTCAGT      1980
132 TGTACTCAA AGGATGGTAA GTTGCTTGCC GATTCTGGTA CAATATCTTA AATTATTGGT      2040
134 TTTTAGATCT GCAACGCACT CATTGATCGT CCAAATACTT TATTCGTATT TGATGACGTA      2100
136 GTTCAAGAAG AAACAATTCT TTGGGCTCAG GAGCTACGTC TTCGATGTCT TGTAACACTT      2160
138 CGTGACGTGG AAATATCAAA TGCTGCTTCT CAAACATGCG AATTCATTGA AGTGACATCA      2220
140 TTGGAATCG ATGAATGTTA TGATTTTCTA GAAGCTTATG GAATGCCGAT GCCTGTTGGA      2280
142 GAAAAAGAAG AAGATGTGCT TAATAAAACA ATCGAACTAA GCAGTGGAAG TCCAGCAACG      2340
144 CTTATGATGT TTTTCAAGTC TTGTGAACCG AAAACATTTG AAAAGTGAGT GGGACATACC      2400
146 AATTTGAGAC TTTTAAAATA ATTTATTCTA CAATAAAAGT TAATCAAAAA GTTTCATAGC      2460
148 TGATTGTCTT TAAATTTTAC GAATTGAGGA TCAAAATCAA GAATTAGGAT CCTGGCACGA      2520
150 GAGAAAACGT TGATGCTACC GTACCCGAGA GATTTTCTTG ATATTTGCCA TCGATTTAAT      2580
152 TTTTAAAGAA AATTATCGTT TTACATAATT GAACAAGAGA TACACGGTCT CGACCCGACG      2640
154 GAAATTTTTT AAATGAAAGC GAGTATGAGC CTGTTTTTCAT TATTTTTCGA TTTTCTCTTG      2700

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```

156 TTGTTTCTTT TTATTTAAAG CCTTTTATTT TGAAACAAGT CTAAAAATAT TAAAACTGA 2760
158 ATAAAAATATT TAAAAAAAT CAAGTAAAAT AGAAAAACAG CAAGGCTGGA GACTACTGTA 2820
160 CTTCTTAAAT CCGCATACTC TTTTATTTA ATCATTTCCT GGAATGTCGA AACGAAATAA 2880
162 TACATTTTGA GTCCAAAATC GCTAGGTATA TTCTTAAAT TATCAAACAT TTTGCATTCA 2940
164 GAATGGCACA GCTTAATAAC AAATTGGAAG GTCGAGGATT AGTCGGTGTT GAATGTATCA 3000
166 CCCCTTACTC GTACAAGTCA CTCGCAATGG CTCTTCAAAG ATGTGTTGAA GTTTTGTCAG 3060
168 ATGAGGATCG AAGTGCTCTT GCTTTCGCAG TTGTGATGCC TCCTGGAGTT GATATACCCG 3120
170 TCAAGCTATG GTCATGTGTT ATTCCAGTTG ATATTTGTTT AAATGAAGAA GAACAATTGG 3180
172 ATGATGAAGT TGCGGATCGG TTGAAAAGAC TCAGCAAGTA TGAGTCTTGA AATTGAAGA 3240
174 TTTAAATTA CACTTAAAT TTCAGACGTG GAGCTCTTCT CAGTGGAAAA CGAATGCCCG 3300
176 TTTTGACATT CAAAATTGAT CATATTATCC ATATGTTCTT GAAACACGTC GTTGATGCAC 3360
178 AAATATCGC CGTATGCTGA AAATGTCTCA ACTTTCAATT AAATTTTAAA TTTTCAGAAT 3420
180 GGAATCTCAA TTCTCGAGCA GCGTCTTCTT GAAATAGGAA ACAATAATGT ATCAGTACCG 3480
182 GAGCGACATA TACCATCACA TTTCCAAAAA TTCCGTCGTT CATCAGCCAG TGAGATGTAT 3540
184 CCAAAAACTA CAGAAGAAAC TGTGATCCGT CCTGAAGACT TCCCAAAGTT CATGCAATTG 3600
186 CACCAGAAAT TCTATGACTC CCTCAAAAAT TTTGCATGCT GTTAAAACCT ATCGTGTACA 3660
188 ATATTGCCTG TATATTCCCC TCGAAATACG TTTATACTTT TTCGCACGAG TTTTCTCATT 3720
190 TTTTCATTG TACTTGTTTT ATTTCTCTCC AAAATTTTCA ATCTATCCCA AATGTTCTTA 3780
192 AATTTAATGT TTTCTACAGA TACTCAACAC ATCTTGTTTC ATCTCATCCT TGCTTTTTTT 3840
194 TTTCAAATAT ATTCAGTTTC TTTTATAATT TTAATTAATC GAATTAATAC ATTCACGTAA 3900
196 AGAATTTTGT GGACTATTAT TTTATCGCAT CCAATGATT TATCCCTAT TGTTGAAAC 3960
198 TTCAAATTG ATCATTTTTA AACACGCCTC ATTAAATTGA AAGTCGTACT TTTAGTCTCG 4020
200 AACATGAAGT AAGTTATTTT CTGTGTTCTA AATTCAAAGT GCATTCCAAA AGGACATTTG 4080
202 ATGAGTTTTT ACGAAAACCG TAATTTTTTAC AATTTCTTTT CAGTTTTGAA GATGTTTCAT 4140
204 TTCTTTCTC TGTTGGCGTC ATTACTACAT TTGCTTTGCT GCTTCACTTT ATCGAGATTC 4200
206 TTGCCATCAA TGGAGTTCCA TCTAGACCGA TAGCAGTCTT CATATCATT TCCCTGTATA 4260
208 TTGTACTGTT TCAGTATTTT AACTTATCGA TTACGTACTA TATTCAGTGG TTCACTGTTT 4320
210 TCGGTCAATG GGTGACACGT GCTCGACGAN NAATTTTCAA CGAACGCAAT CTCCTAGTCA 4380
212 CTTATCAACC AAGAGCCCTC ACCCATG 4407

```

## 214 (2) INFORMATION FOR SEQ ID NO: 2:

## 216 (i) SEQUENCE CHARACTERISTICS:

217 (A) LENGTH: 549 amino acids

218 (B) TYPE: amino acid

219 (C) STRANDEDNESS: Not Relevant

220 (D) TOPOLOGY: linear

## 222 (ii) MOLECULE TYPE: protein

## 224 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

226 Met Leu Cys Glu Ile Glu Cys Arg Ala Leu Ser Thr Ala His Thr Arg
227 1 5 10 15
229 Leu Ile His Asp Phe Glu Pro Arg Asp Ala Leu Thr Tyr Leu Glu Gly
230 20 25 30
232 Lys Asn Ile Phe Thr Glu Asp His Ser Glu Leu Ile Ser Lys Met Ser
233 35 40 45
235 Thr Arg Leu Glu Arg Ile Ala Asn Phe Leu Arg Ile Tyr Arg Arg Gln
236 50 55 60
238 Ala Ser Glu Leu Gly Pro Leu Ile Asp Phe Phe Asn Tyr Asn Asn Gln
239 65 70 75 80
241 Ser His Leu Ala Asp Phe Leu Glu Asp Tyr Ile Asp Phe Ala Ile Asn
242 85 90 95

```

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Output Set: N:\CRF4\03102003\H984178.raw

```

244   Glu Pro Asp Leu Leu Arg Pro Val Val Ile Ala Pro Gln Phe Ser Arg
245           100                      105                      110
247   Gln Met Leu Asp Arg Lys Leu Leu Leu Gly Asn Val Pro Lys Gln Met
248           115                      120                      125
250   Thr Cys Tyr Ile Arg Glu Tyr His Val Asp Arg Val Ile Lys Lys Leu
251           130                      135                      140
253   Asp Glu Met Cys Asp Leu Asp Ser Phe Phe Leu Phe Leu His Gly Arg
254           145                      150                      155                      160
256   Ala Gly Ser Gly Lys Ser Val Ile Ala Ser Gln Ala Leu Ser Lys Ser
257           165                      170                      175
259   Asp Gln Leu Ile Gly Ile Asn Tyr Asp Ser Ile Val Trp Leu Lys Asp
260           180                      185                      190
262   Ser Gly Thr Ala Pro Lys Ser Thr Phe Asp Leu Phe Thr Asp Ile Leu
263           195                      200                      205
265   Leu Met Leu Lys Ser Glu Asp Leu Leu Asn Phe Pro Ser Val Glu
266           210                      215                      220
268   His Val Thr Ser Val Val Leu Lys Arg Met Ile Cys Asn Ala Leu Ile
269           225                      230                      235                      240
271   Asp Arg Pro Asn Thr Leu Phe Val Phe Asp Asp Val Val Gln Glu Glu
272           245                      250                      255
274   Thr Ile Arg Trp Ala Gln Glu Leu Arg Leu Arg Cys Leu Val Thr Thr
275           260                      265                      270
277   Arg Asp Val Glu Ile Ser Asn Ala Ala Ser Gln Thr Cys Glu Phe Ile
278           275                      280                      285
280   Glu Val Thr Ser Leu Glu Ile Asp Glu Cys Tyr Asp Phe Leu Glu Ala
281           290                      295                      300
283   Tyr Gly Met Pro Met Pro Val Gly Glu Lys Glu Glu Asp Val Leu Asn
284           305                      310                      315                      320
286   Lys Thr Ile Glu Leu Ser Ser Gly Asn Pro Ala Thr Leu Met Met Phe
287           325                      330                      335
289   Phe Lys Ser Cys Glu Pro Lys Thr Phe Glu Lys Met Ala Gln Leu Asn
290           340                      345                      350
292   Asn Lys Leu Glu Ser Arg Gly Leu Val Gly Val Glu Cys Ile Thr Pro
293           355                      360                      365
295   Tyr Ser Tyr Lys Ser Leu Ala Met Ala Leu Gln Arg Cys Val Glu Val
296           370                      375                      380
298   Leu Ser Asp Glu Asp Arg Ser Ala Leu Ala Phe Ala Val Val Met Pro
299           385                      390                      395                      400
301   Pro Gly Val Asp Ile Pro Val Lys Leu Trp Ser Cys Val Ile Pro Val
302           405                      410                      415
304   Asp Ile Cys Ser Asn Glu Glu Glu Gln Leu Asp Asp Glu Val Ala Asp
305           420                      425                      430
307   Arg Leu Lys Arg Leu Ser Lys Arg Gly Ala Leu Leu Ser Gly Lys Arg
308           435                      440                      445
310   Met Pro Val Leu Thr Phe Lys Ile Asp His Ile Ile His Met Phe Leu
311           450                      455                      460
313   Lys His Val Val Asp Ala Gln Thr Ile Ala Asn Gly Ile Ser Ile Leu
314           465                      470                      475                      480
316   Glu Gln Arg Leu Leu Glu Ile Gly Asn Asn Asn Val Ser Val Pro Glu

```

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```

317           485           490           495
319   Arg His Ile Pro Ser His Phe Gln Lys Phe Arg Arg Ser Ser Ala Ser
320           500           505           510
322   Glu Met Tyr Pro Lys Thr Thr Glu Glu Thr Val Ile Arg Pro Glu Asp
323           515           520           525
325   Phe Pro Lys Phe Met Gln Leu His Gln Lys Phe Tyr Asp Ser Leu Lys
326           530           535           540
328   Asn Phe Ala Cys Cys
329           545
331 (2) INFORMATION FOR SEQ ID NO: 3:
332   (i) SEQUENCE CHARACTERISTICS:
333       (A) LENGTH: 12 amino acids
334       (B) TYPE: amino acid
335       (C) STRANDEDNESS: Not Relevant
336       (D) TOPOLOGY: linear
337   (ii) MOLECULE TYPE: protein
341   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
342   Asp Gln Asp Lys Ser Gly Phe Ile Glu Glu Asp Glu
343   1           5           10
346 (2) INFORMATION FOR SEQ ID NO: 4:
347   (i) SEQUENCE CHARACTERISTICS:
348       (A) LENGTH: 12 amino acids
349       (B) TYPE: amino acid
350       (C) STRANDEDNESS: Not Relevant
351       (D) TOPOLOGY: linear
352   (ii) MOLECULE TYPE: protein
356   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
357   Asp Gln Asp Lys Asp Asp Phe Ile Gly Glu Asp Glu
358   1           5           10
361 (2) INFORMATION FOR SEQ ID NO: 5:
362   (i) SEQUENCE CHARACTERISTICS:
363       (A) LENGTH: 12 amino acids
364       (B) TYPE: amino acid
365       (C) STRANDEDNESS: Not Relevant
366       (D) TOPOLOGY: linear
367   (ii) MOLECULE TYPE: protein
371   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
372   Asp Ser Asp Gly Asp His Lys Ile Gly Val Asp Glu
373   1           5           10
376 (2) INFORMATION FOR SEQ ID NO: 6:
377   (i) SEQUENCE CHARACTERISTICS:
378       (A) LENGTH: 12 amino acids
379       (B) TYPE: amino acid
380       (C) STRANDEDNESS: Not Relevant
381       (D) TOPOLOGY: linear
382   (ii) MOLECULE TYPE: protein
386   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
387   Asp Ile Asn Lys Asp Asp Val Val Ser Trp Glu Glu
388   1           5           10
389

```

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/08/984,178

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TIME: 15:40:05

Input Set : N:\Crf3\RULE60\08984178.RAW.txt  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 4350,4351

Seq#:20; Xaa Pos.94,95,96,120,179,318

Seq#:21; Xaa Pos.310

## VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\08984178.RAW.txt

Output Set: N:\CRF4\03102003\H984178.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:35 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)  
L:62 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1  
L:457 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=11  
L:564 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=18  
L:959 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:80  
M:341 Repeated in SeqNo=20  
L:1109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:304  
L:1150 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=22  
L:1164 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=23  
L:1178 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=24  
L:1192 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=25  
L:1206 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=26  
L:1220 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=27  
L:1234 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=28